IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Ramnarayan *et al.*

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For: *USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS*

Art Unit: 1631

Examiner: Brusca, J.

MARKED-UP CLAIMS (37 CFR §1.121)

IN THE CLAIMS:

Please amend claim 23 as follows:

23. (Amended) A computer-based method for predicting clinical responses in patients based on genetic polymorphisms, comprising:

obtaining one or more amino acid sequences for a target protein that is the product of a gene exhibiting genetic polymorphisms;

generating 3-D protein structural variant models from the sequences;

building a relational database of protein structural variants [derived] based on genetic polymorphisms and observed clinical data associated with particular polymorphisms exhibited in the patients, wherein the database comprises:

3-D molecular coordinates for [the] structural variant-drug complex models;

[a molecular graphics interface for 3-D molecular structure visualization;

functionality for protein sequence and structural analysis;

database searching tools;] and

observed clinical data associated with the genetic polymorphisms;

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obtaining a target protein structural variant [based on the same]<u>encoded by a</u> gene [associated with a polymorphism]<u>exhibiting genetic polymorphism</u> in a patient;

generating a 3-D protein model based on the [subject's]<u>patient's</u> gene sequence;

[screening/comparing]<u>screening or comparing</u> the 3-D model derived from the [subject]<u>patient</u> to the structures contained in the database by:

identifying structures in the database that are similar to the model derived from the [subject]<u>patient</u>; and

predicting a clinical outcome for the patient based on the clinical data associated with the identified structures.